



Replacement Sheet

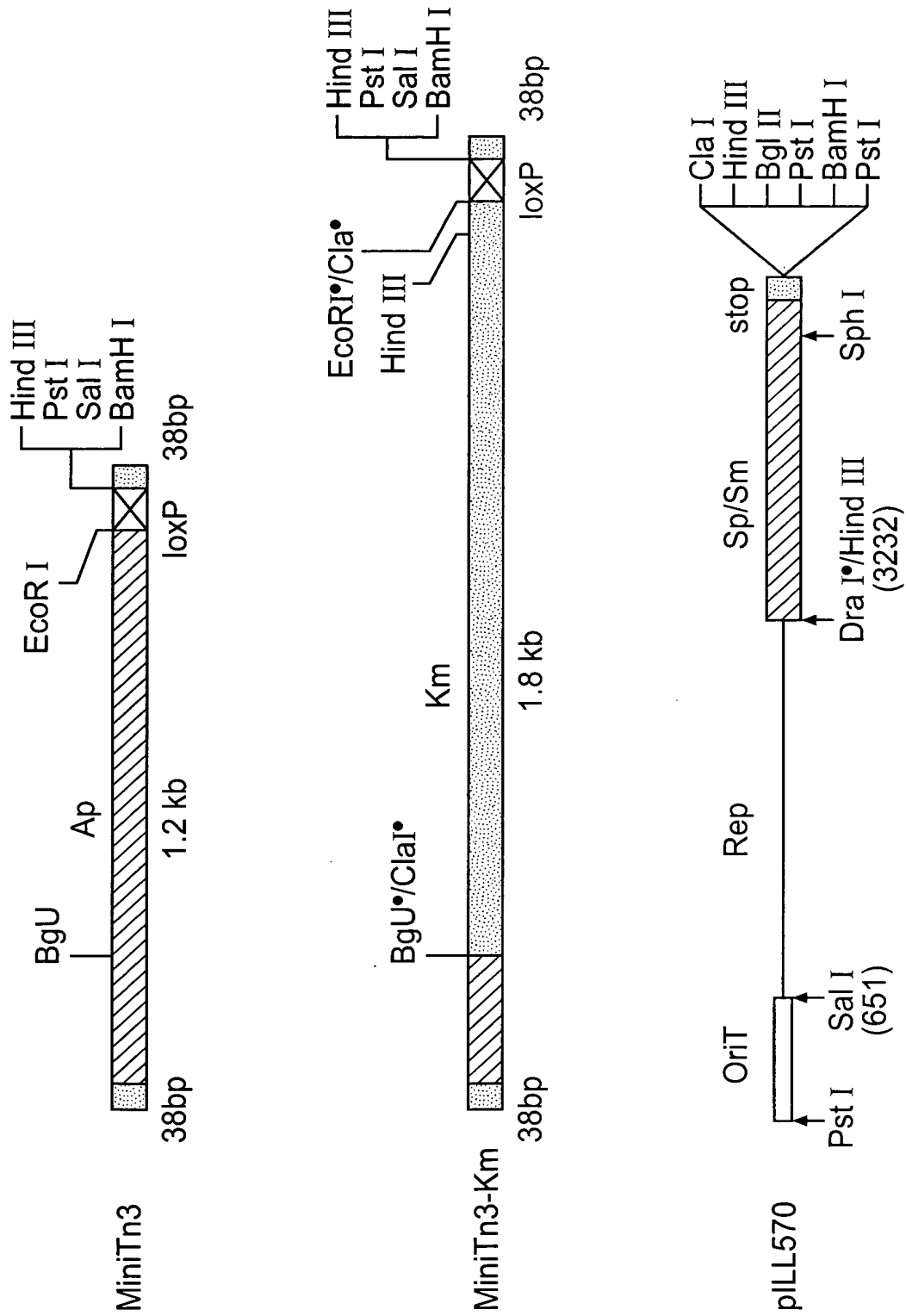


FIG. 1A



Replacement Sheet

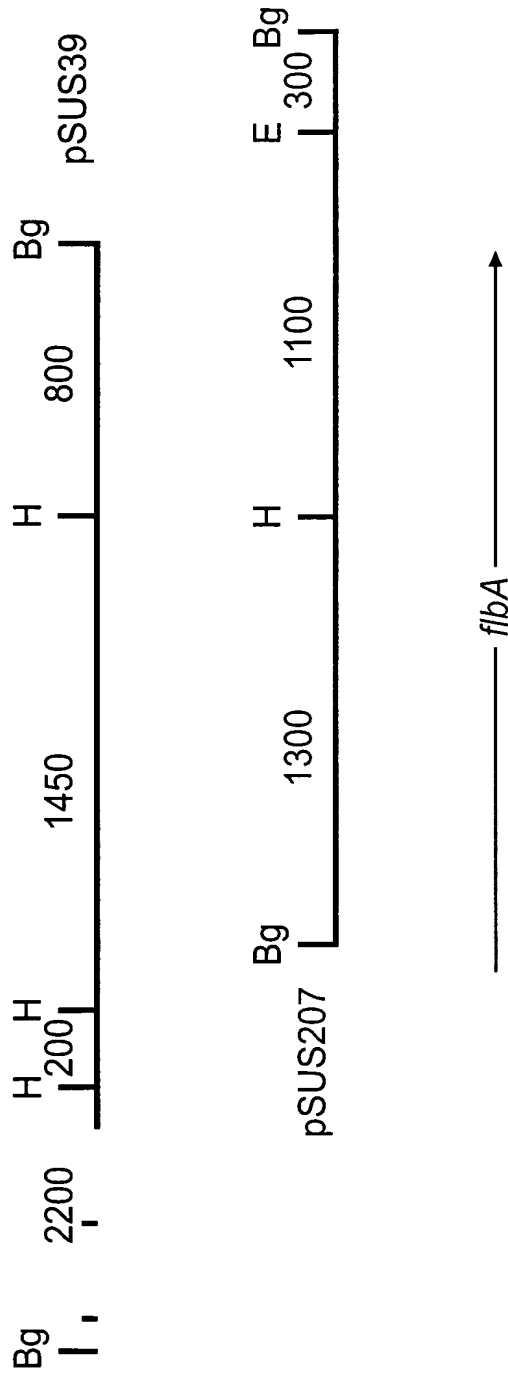


FIG. 1B



Replacement Sheet

1	AGC	TTT	TTT	GTG	CCA	TAC	TTT	TAA	ACT	TTA	TAT	AAT	AAG	AGA	CAA	ACA	CAC	CTA	CCA	31	
61	AAA	TTA	AGG	CAT	TGA	TTT	TAG	ATT	ATG	GCA	AAC	GAA	CGC	TCC	AAA	TTA	GCT	TTT	AAA	AAG	91
121	ACT	TTC	CCT	GTC	TTT	AAA	CGC	TTC	TTG	CAA	TCC	AAA	GAC	TTA	GCC	CTT	GTG	GTC	TTT	GTG	151
181	T	F	P	V	F	K	R	F	L	Q	S	K	D	L	A	L	V	V	F	V	211
241	ATA	GCG	ATT	TTA	GCG	ATC	ATT	ATC	GTG	CCG	TTA	CCG	CCT	TTT	GTG	TTG	GAT	TTT	TTA	CTC	271
301	ACG	ATT	TCT	ATC	GCG	CTA	TCG	GTG	TTG	ATT	ATT	TTA	ATC	GGG	CTT	TAT	ATT	GAC	AAA	CCG	331
361	ACT	GAT	TTT	AGC	GCT	TTC	CCC	ACT	TTA	TTA	CTC	ATT	GTA	ACC	TTA	TAC	CGC	TTG	GCT	TTA	391
421	AAT	GTC	GCC	ACC	ACT	AGA	ATG	ATT	TTA	ACC	CAA	GGC	TAT	AAA	GGG	CCT	AGC	GCG	GTG	AGC	451
	N	V	A	T	T	R	M	I	L	T	Q	G	Y	K	G	P	S	A	V	S	
	ATT	ATC	ACG	GCG	TTT	GGG	GAA	TTT	AGC	GTG	AGC	GGG	AAT	TAT	GTG	ATT	GGG	GCT	ATT		
	I	I	I	T	A	F	G	E	F	S	V	S	G	N	Y	V	I	G	A	I	

FIG. 2A



Replacement Sheet

481	ATC	TTT	AGT	ATT	TTA	GTG	CTG	GTG	AAT	TTA	TTA	GTG	GTT	ACT	AAT	GGT	TCT	ACT	AGG	GTT
	I	F	S	I	L	V	L	V	N	L	L	V	V	T	N	G	S	T	R	V
541	ACT	GAA	GTT	AGG	GCG	CGA	TTT	GCC	CTA	GAC	GCT	ATG	CCA	GGA	AAG	CAA	ATG	GCG	ATT	GAT
	T	E	V	R	A	R	F	A	L	D	A	M	P	G	K	Q	M	A	I	D
601	GCG	GAT	TTA	AAT	TCA	GGG	CTT	ATT	GAT	GAT	AAG	GAA	GCT	AAA	AAA	CGG	CGC	GCC	GCT	CTA
	A	D	L	N	S	G	L	I	D	D	K	E	A	K	K	R	R	A	A	L
661	AGC	CAA	GAA	GCG	GAT	TTT	TAT	GGT	GCG	ATG	GAT	GGC	GCG	TCT	AAA	TTT	GTC	AAA	GGC	GAT
	S	Q	E	A	D	F	Y	G	A	M	D	G	A	S	K	F	V	K	G	D
721	GCG	ATC	GCT	TCT	ATC	ATT	ATC	ACG	CTT	ATC	AAT	ATC	ATT	GGG	GGT	TTT	TTA	GTG	GGC	GTG
	A	I	A	S	I	I	I	T	L	I	N	I	I	G	G	F	L	V	G	V
781	TTC	CAA	AGG	GAT	ATG	AGC	TTG	AGC	TTT	AGT	GCT	AGC	ACT	TTC	ACT	ATC	TTA	ACC	ATT	GGC
	F	Q	R	D	M	S	L	S	F	S	A	S	T	F	T	I	L	T	I	G
841	GAT	GGG	CTT	GTA	GGG	CAA	ATC	CCT	GCC	TTA	ATC	ATT	GCG	ACA	CGG	ACC	GGT	ATT	GTC	GCC
	D	G	L	V	G	Q	I	P	A	L	I	I	A	T	R	T	G	I	V	A
901	ACT	CGC	ACC	ACG	CAA	AAC	GAA	GAA	GAG	GAC	TTT	GCT	TCT	AAG	CTC	ATC	ACA	CAG	CTC	ACC
	T	R	T	T	Q	N	E	E	E	D	F	A	S	K	L	I	T	Q	L	T

FIG. 2B



Replacement Sheet

961 AAT AAA AGC AAA ACT TTA GTG ATT GTG GGG GCG ATT TAT TGC TTT TGC ACC ATT CCT GGA
N K S K T L V I V G A I Y C F C T I P G
1021 CTC CCT ACC TTT TCT TTA GCG TTT GTA GGG GCT CTC TTT TTA TTC ATC GCA TGG CTG ATT
L P T F S L A F V G A L F L F I A W L I
1081 AGC AGG GAG GGA AAG GAC GGG TTG CTC ACT AAA TTA GAA AAT TAT TTG AGT CAA AAA TTC
S R E G K D G G L L T T K L E N Y L S Q K F
1141 GGC TTG GAT TTG AGC GAA AAA CCC CAC AGC TCC AAA ATC AAA CCC CAC GCC CCC ACC ACA
G L D L S E K P H S S K I K P H A P T T
1201 AGG GCT AAA ACC CAA GAG ATT AAA AGA GAA GAG CAA GCC ATT GAT GAA GTG TTA
R A K T Q E E I K R E E Q A I D E V L
1261 AAA ATT GAA TTT TTA GAA TTG GCT TTA GGC TAT CAG CTC TAC AGC TTA GCG GAC ATG AAA
K I E F L L E L A L G Y Q L Y S L A D M K
1321 CAA GGG GGC GAT TTG TTA GAA AGG ATT AGG GGT ATT AGA AAA AAG ATA GCG AGC GAT TAT
Q G G D L L E R I R R G I R K K I A S D Y
1381 GGT TTT TTG ATG CCT CAA ATT AGG ATT AGG GAT AAT TTA CAA CTC CCC CCA ACG CAT TAT
G F L M P Q I R I R D N L Q L P T H Y

FIG. 2C



Replacement Sheet

1441 GAA ATC AAG CTT AAG GGC ATT GTG ATT GGT GAA GGC ATG GTG ATG CCG GAT AAG TTT TTA
E I K L K G I V I G G E G M V M P Q K F L
1501 GCC ATG AAT ACC GGT TTT GTG AAT AAA GAA ATT GAA GGC ATT CCT ACT AAA GAG CCG GCT
A M N T G G F V N K E I E G I P T K E P A
1561 TTT GGA ATG GAC GCT TTA TGG ATT GAA ACT AAA AAT AAA GAA GCC ATC ATT CAA GGC
F G M D A L W I E T K N K E E A I I Q G
1621 TAT ACC ATT ATT GAT CCA AGC ACC GTT ATT GCG ACG CAC ACC AGC GAA TTA GTG AAA AAA
Y T I I D P S T V I A T H T S E L V K K
1681 TAC GCT GAA GAT TTT ATC ACT AAA GAT GAA GTG AAA TCC CTT TTA GAG CGC TTG GCC AAA
Y A E D F I T K D E V K K I P S L L E R L A K
1741/581 GAC TAT CCT ACG ATT GTA GAA GAG AGT AAA AAT ATC CCC ACC GGT GCG ATC CGA TCA GTC
D Y P T I V E E S K I P T G A I R S V
1801 TTG CAA GCC TTG TTG CAT GAA AAA ATC CCC ATT AAA GAC ATG CTC ACT ATT TTA GAA ACG
L Q A L L H E K I P I K D M L T I L E T
1861 ATT ACC GAT ATT GCG CCA TTA GTT CAA AAC GAT GTG AAT ATC TTA ACC GAA CAA GTG AGG
I T D I A P L V Q N D V N I L T E Q V R

FIG. 2D



Replacement Sheet

1921	GCG	AGG	CTT	TCT	AGG	GTG	ATC	ACT	AAC	GCT	TTT	AAA	TCT	GAA	GAC	GGG	CGT	TTG	AAA	TTT
A	R	L	S	R	V	I	T	N	A	F	K	S	E	D	G	R	L	K	F	
1981	TTA	ACC	TTT	TCT	ACC	GAT	AGC	GAA	CAA	TTT	TTG	CTT	AAT	AAA	TTG	CGA	GAA	AAT	GGC	ACT
L	T	F	S	T	D	S	E	Q	F	L	L	N	K	L	R	E	N	G	T	
2041	TCT	AAG	AGC	CTA	CTA	CTC	AAT	GTG	GGC	GAA	TTG	CAA	AAA	CTC	ATT	GAA	GCG	GTC	TCT	GAA
S	K	S	L	L	L	N	V	G	E	L	Q	K	L	I	E	A	V	S	E	
2101	GAG	GCC	ATG	AAA	GTC	TTG	CAA	AAA	GGG	ATC	GCT	CCG	GTG	ATT	TTG	ATC	GTA	GAG	CCT	AAT
E	A	M	K	V	L	Q	K	G	I	A	P	V	I	L	L	I	V	E	P	N
2161	TTA	AGA	AAA	GCC	CTT	TCT	AAT	CAA	ATG	GAG	CAG	GCT	AGG	ATT	GAT	GTA	ATC	GTG	CTA	AGC
L	R	K	A	L	S	N	Q	M	E	Q	A	R	I	D	V	I	V	L	S	
2221	CAT	GCT	GAA	TTA	GAT	CCT	AAC	TCT	AAT	TTT	GAA	GCC	TTA	GGC	ACG	ATC	CAT	ATT	AAC	TTT
H	A	E	L	D	P	N	S	N	F	E	A	L	G	T	I	H	I	N	F	
2281	TAA	GGG	ATA	AAT	AAT	TGA	TAA	AAA	AGG	AGA	ATG	ATG	CAA	GTT	TAT	CAC	CTT	TCA	CAC	ATT
2341	GAT	TTA	GAC	GGC	TAT	GCA	TGC	CAG	CTT	GTT	TCA	AAA	CAA	TTT	TTT	AAA	AAT	ATC	CAA	TGC
2401	TAT	AAC	GCT	AAT	TAC	GGG	CGT	GAA	GTC	TCA	GCG	AGA	ATT	TAT	GAG	ATT	TTA	AAC	GCG	ATC
2461	GCT	CAA	TCT	AAA	GAG	AGT	GAA	TTC	CTT	ATT	TTG	ATT	AGC	GA						

FIG. 2E



Replacement Sheet

1 MANKRS-KLAFKKTFPVFKRFLQSKDLALVVFVIAIALAIIIVPLPPFVLDFFLLTISIALS HpFlba
1 MAKNKIVDLVFPFLGPLIAPVLKAKSLTIVGFLVCILAIIVPLPSPILDFFLALSIALS CjFlba
1 MADAAAPNASSMPSAKSLDGLMRGEMGLAGVVGIIIVLLIIPVPAPLLDVLLAISLTGS CcFlbF
1 -----MNPHDLEWLNRIGERKDIMLAVLLAVVFMVLPPLPVLVDILIAVNMTIS YpLcrD
1 -----MLLSLNSARLRPRLLILVLMVMIISMFVIPLPTYLVDFLIALNIVLA StInva
1 -----MVMIIAMLIIPPTYLVDFLIGLNIVLA SfmXia

60 VLIILIGLYIDKPTDFSAPTLLIVTLYRLALNVATTRMILLTQGYKGPSAVSIIITAFG HpFlba
61 VLIILISIIYIPKPTDLTTFPTLLIITLFRLSLNIATTRMILLSEGQNGPEAVSEIIAAFG CjFlba
61 VLIIMTAIILIKKPLEFTSFPTVLLVTTLFRGLNIASTRLLILSHGQEGTGAGAVIEAFG CcFlbF
52 VVLLMIAIYINSPLOFSAPPAVLLVTTLFRALSSTTRMILLQ-----ADAGQIVYTFG YpLcrD
49 ILVFMGSFYIDRILSFSTFPAVLLITTLFRALSISTSRLLILIEA-----DAGEIIATFG StInva
29 ILVFMGSFYIERILSFSTFPSVLLITTLFRALSISTSRLLILVDADRKG-----IITTFG SfmXia
.. * . . . * * *

120 EFSVSGNYVIGAIIFSILVLVNLVVTNGSTRVTEVRARFALDAMPKGQMAIDADLNSGL HpFlba
121 EFVVGGNMVIGVIVFCILVLINFMVVTKGSTRVSEVQARFTLDAMPKGQMAIDADLNAGL CjFlba
121 HLMMQGNFVIGVIVFIILIVNFMVVTKGSGRIAEVAARFTLDSMPKGQMAIDADLSTGL CcFlbF
107 NFVVGGNLIVGIVIFLIITIVQFLVITKGSERVAEVSARFSLDAMPGKOMSIDGDMRAGV YpLcrD
104 QFVIGDSLAVGVVFSIVTVVQFIVITKGSERVAEVAARFSLDGMFGKQMSIDADLKAGI StInva
84 QFVIGDSLAVGVVFSIVTVVQFIVITKGSERVAEVAARFSLDGMFGKQMSIDADLKAGI SfmXia
.. . . * * * . . . * * * * * * * * * * * *

FIG. 3A



Replacement Sheet

180	IDDKEAKKRRRAALSQEADFYGAMDGASKFVKGDAlASIIITLNIIGGFLVGVFQRDMSL	HpFlba
181	IDEQTARARRQEVIAEANFYGAMDGSSKFIKGDVAVAGIIITIIINIIIGGFLIGSFQHDMAL	CjFlba
181	ISQDEAKIRRKELEQESTFFGAMDGASKFVKGDAlAGLIITAINIIGGIIIGVVQHKMPF	CcFlbF
167	IDVNEARERRATIEKESQMFSGMDGAMKFKGDAlAGLIIFVNIILGGVTIGVTQKGLAA	YpLcrD
164	IDADAARERRSVLERESQLYGSFDDGAMKFKGDAlAGIIIFVNFIIIGGISVGMTRHGMDL	StInva
144	IDAAGAKERRSILERESQLYGSFDDGAMKFKGDAlAGIIIFVNLIIIGGISVGMSQHGMSL	SfMxia
	* . * * . . * . * * * * * * * * * *	
240	SFSASTFTILTIGDGLVGQIPALIIATRTGIVATRTTQNEEEDFASKLITQLTNKSKTLV	HpFlba
241	SDAASTYTLTIGDGLVSQIPGLITSTATAIIITRASKDEENFAEGTLTQLLSEYRTLII	CjFlba
241	GDAASTYTIMTIGDGLVSQIPALIIISIAAGMVSKAGVEGSADKALTQLAMNPVGLGMV	CcFlbF
227	AEALQLYSILTVGDGMVSQVPALLIAITAGIIVTRVSSDSDLGSDIGKQVVAQPKAML	YpLcrD
224	SSALSTYTMLTIGDGLVAQIPALLIAISAGFIVTRVNGDTDN-MGRNIMTQLLNNPFVLV	StInva
204	SGALSTYTLTIGDGLVSQIPALLISISAGFMLTRVNGDSDN-MGRNIMSQIFGNPFVLI	SfMxia
 * * * * *	
300	IVGAIYC-FCTIPGLPTFSLAFVGALFLFIAWLISREGKDGLLTKLENYLSQKFGLDLSE	HpFlba
301	VGfVLFI-FALVPGLPTLSLGFMALVFLSLGYLTkQVKEGKI----DITTVKKSKPSAA	CjFlba
301	SASSG-I-IALIPGMPIFPFAAMALA-----AGALAY	CcFlbF
287	IGVLLLLFGLIPGFPTVTLILALLVCGGGMVLSRKQSRNDEANQDLQSLTSGGAPA	YpLcrD
283	VTAILTISMGTLPGFPLPVFVILSVLSVLFFYKFKREAKRSAAPKTSKGEQPLSIEEKE	StInva
263	VTSALALAIGMLPGFPFFVFFLIAVTLTALFYKKVVEKEKSLSESDSSGYTG-----	SfMxia
	* * *	

FIG. 3B



Replacement Sheet

359 KPHSSKIKPHAPTTRAKTQEEIKREEEQAIDEVLKIEFLELALGYQLYSLADMKQGGDLL HpFlba
355 VASQSGAGTTAAPAKKSEEEIILKEEHKINDILKVEILELELGYGLIKLAE---NLT CjFlba
331 KRVQDAKKPKALDPADLEAAAPSEPEEPISASLAIDDVKIELGYGLLTINDLDGRKLT CcFlbF
347 ARTKAKTSGANKGRIDGEQAFAMTVPLIIDVDS-----SQQEALEANALN YpLcrD
343 GSSLGLIGDLKVSTE-----TVPLIILLVPKSRREDLEKA StInva
316 -----TFDIDNTHDSSLAMIENLDRISSETVPLIILLFAENKINANDME SfmXia
* * *

419 ERIRGIRKKIASDYGFLMPQIRIRDNLQLPPTHYEIKLKGIVIGPMVMPDKFLAMNTGF HpFlba
411 ERIRSMRRSIAESLGLFMPKIRIRDNLRLKPNESYFKLKGVSIAAEIYPDKYLAMDSGF CjFlba
391 DQIRALRKTASEYGFVMPPIILNMRLANQGYAIRIKEMEAGAGEVRLGCLMCDPRG CcFlbF
392 DELVRVRALYLDLGVFPFGIHLRFNEGMEGEYIISLQEVVPARGELKAGYLLVRESVS YpLcrD
378 QLAERLRSQFFIDYGVRLPEVLLRDGEGLDDNSIVLLINEIRVEQFTVYFD--LMRVVNY StInva
359 GLIERIRSQFFIDYGVRLPTILYRTSNEIKVDDIVLLINEVRADSFNIYFDKVCITDENG SfmXia
* * * * *

479 VNKEIEGIPTKEPAF--GMDALWIETKNKEEAI IQGYTIIDPSTVIATHTSELVKKYAED HpFlba
471 ITEEIEGIATKEPAF--NSDALWIDANLKDEATLNGYIVIDPASVISTHMSSELIKAHASE CjFlba
451 GOVELPGEHVREPAF--GLPATWIADDLREEATFRGYTVVDPATVLTTHLTEILKENMAD CcFlbF
452 QLELLGIPYEKGEHLLPDQEAFFWVSVEYEEERLEKSQLEFFSHSQVLTWHLSHVLREYAED YpLcrD
436 SDEVVSFGINPTIHQQSSQYFWVTHEEGERLEKRELGYVLRNALDELYHCLAVTVARNVNE StInva
419 DIDALGIPVSTS--YNERVISWVDVSYTENLTNIDAKIKSAQDEFYHQLSQALLNNINE SfmXia
* * * * *

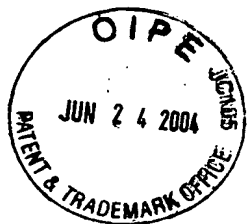
FIG. 3C



Replacement Sheet

537	FITKDEVKSLLERLAKDYPTIVEESK-KI-PTGAIRSVLQALLHEKIPKIDMLTILETIT	HpFlba
529	LLTRQEVQNLKVKNDYPIIVEGAL-GVAPVSLIQILKDLLKHHIPIKIDMLTILESVS	CjFlba
509	LLSYAEVQKLLKELPETQKLLVDDLIPGTVTATTQVRVLSLRERSIRDLPQILEGVG	CcFlbF
512	FIGIOETRYLLEQMEGGYGELIKEVOR-IVPLQRMTEILQRLVGEDISIRNMRISILEAMV	YpLcrD
496	YFGIOETKHMLDQLEAKFPDLLKEVLRH-ATVQRISEVLQRLLSERVSVRNMKLIMEALA	StInva
477	IFGIOETKNMLDQFENRYPDLLKEVFRHV-TIQRISEVLQRLLGENISVRNLKLIMESLA	SfMxia
* *		
595	DIAPLVQNDVNILTEQVRARLSRVITNAPKSEDRGLKFLTFSTDSEQLLNKLRENGTSK	HpFlba
588	DIAR-VSKSFDMIIEKVRASLARMITNMYLDDKGNLDIFILDSASSAVLMENVQFRDGSY	CjFlba
569	EAAPHTA-SVTQLVEQVRARLARQLCWANRGDDGALPIITLSADWEQAFAEALIGPGDDK	CcFlbF
571	EWGQK-EKDVVQLTEYIRSSLKRYICYKANGNNILPAYLFDQOEVEEKIRSGVRQTSAGS	YpLcrD
555	LWAPR-EKDVINLVEHIRGAMARYICHKF-ANGGELRAVMVSAEVEDVIRKGIRQTSGST	StInva
536	LWAPR-EKDVITLVEHVRASSLRYICSK-IAVSGEIKVVMLSGYIEDAIRKGIRQTSGGS	SfMxia
* *		
655	SLLLNVGELQKLI FAVSEEMKVLQKGIAPVILIVEPNLRKALSNQMEQARIDVIVLSHA	HpFlba
647	HLPLSVAQGTGLVDTLRAEVA AVANGRIKPFILCVEPQLRKF IADICYNFSINIVVLSFA	CjFlba
628	QALPPSRLODFIRGVRDSFERAALAGEAPVLL-TSPGVRRPYVRSI IERFRGQTVVMSQN	CcFlbF
630	YLALEPAVTESLLEQVRKTIGDLSQIQSKP-VLIVSMDIRRYVRKLI ESEYYGLPVL SYQ	YpLcrD
613	FLSLDPFASANLMDLITLKLDDLIAH-KDLVLLTSVDVRRFIKKMIEGRFPDLEVL SFG	StInva
594	FLNMDIEVSDEVMETLAHALREL-RNAKKNFVLLVSDIRRFVKRLIDNRFKSILVISYA	SfMxia
* *		
715	ELDPNSNFEALGTIHIINF	HpFlba
707	EIAENTNFNTEGIIRIEL	CjFlba
687	EIHPRARLKTVMV----	CcFlbF
689	ELTQQINIQLGRICL--	YpLcrD
672	EIADSKSVNVIKTI----	StInva
653	EIDEAYTINVLKTI----	SfMxia
* *		

FIG. 3D



Replacement Sheet

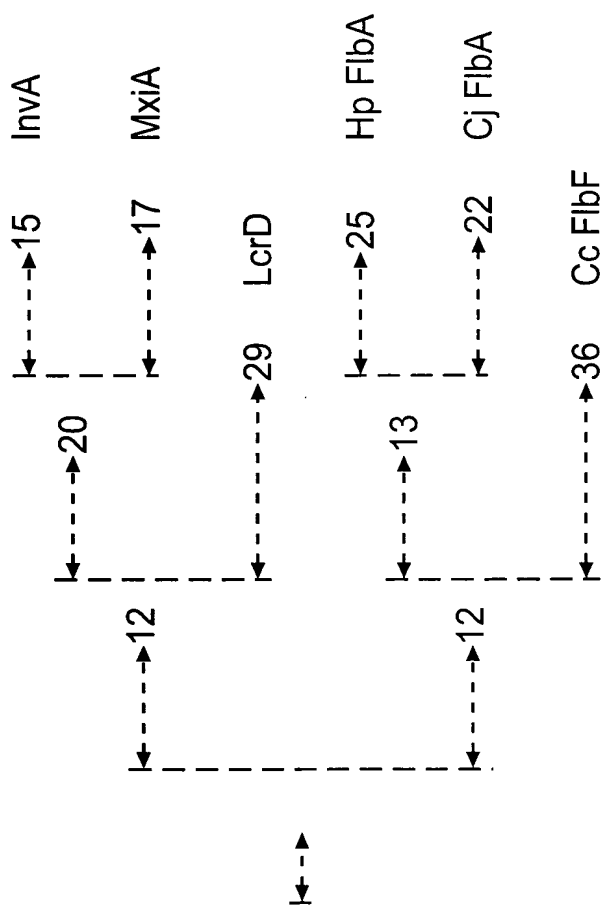
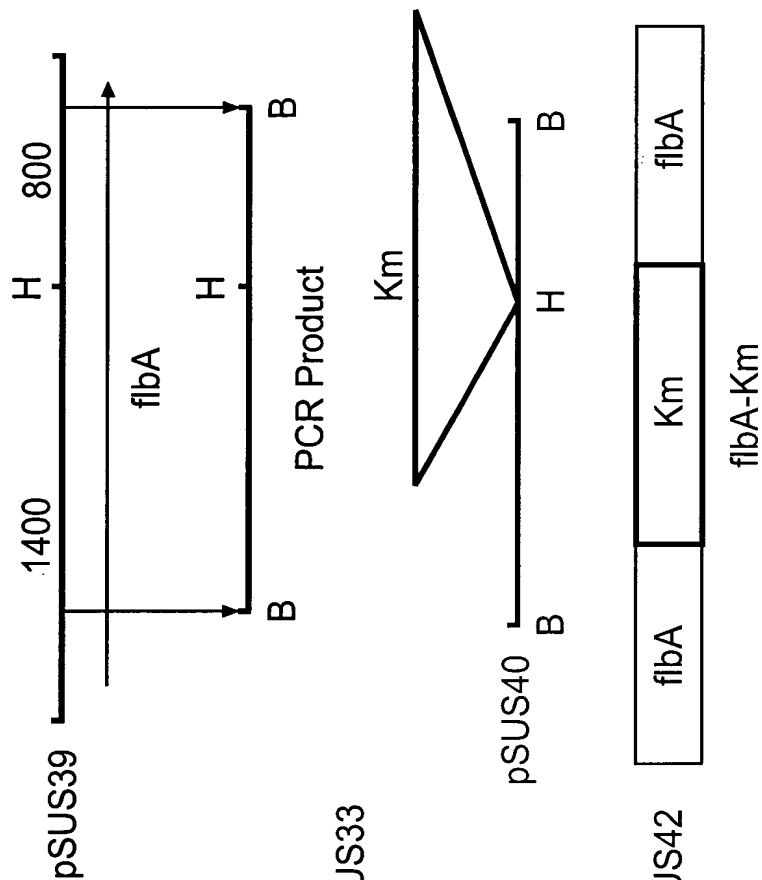


FIG. 4



Replacement Sheet



1) PCR amplification

2) Cloning the PCR product in pSUS33

3) Insertion of the Km cartridge

4) Electroporation in H. pylori N6

FIG. 5



Replacement Sheet

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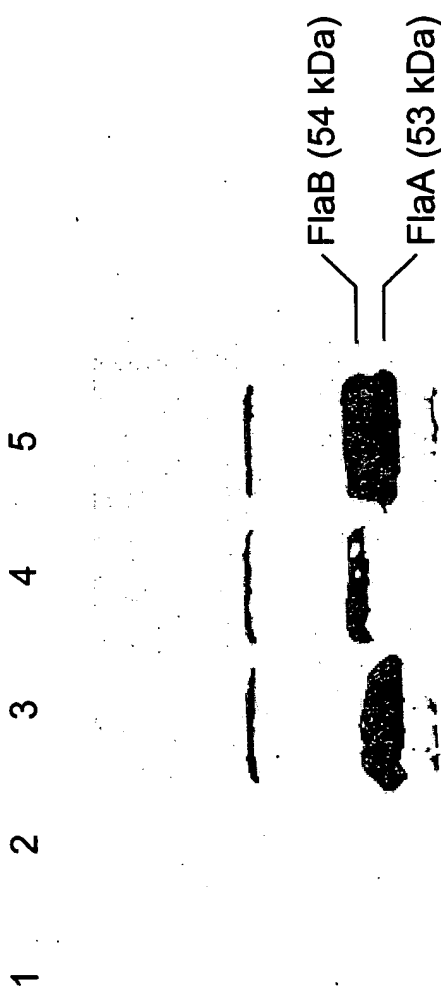


FIG. 6



Replacement Sheet

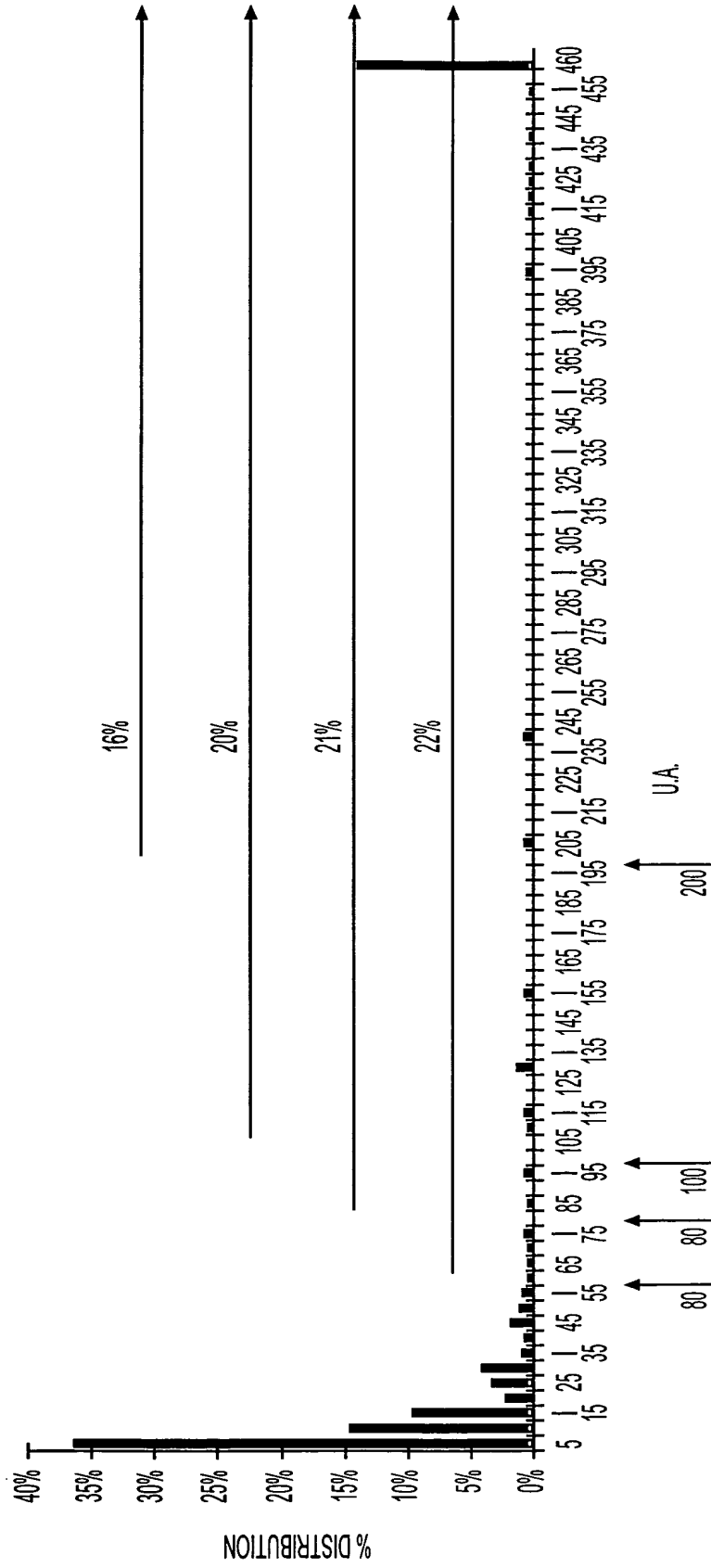
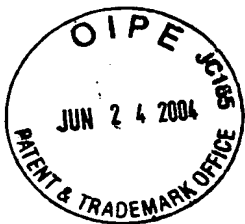


FIG. 7



Replacement Sheet

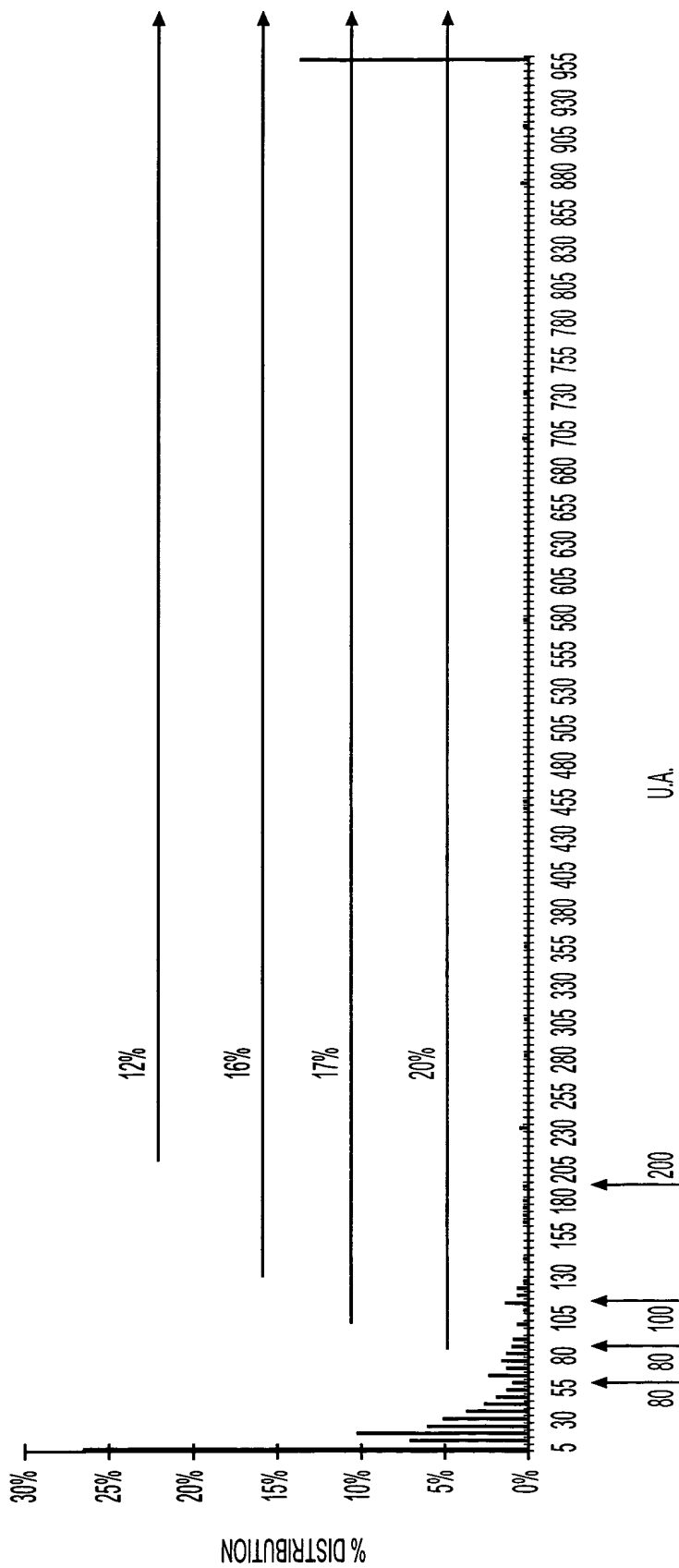


FIG. 8



Replacement Sheet

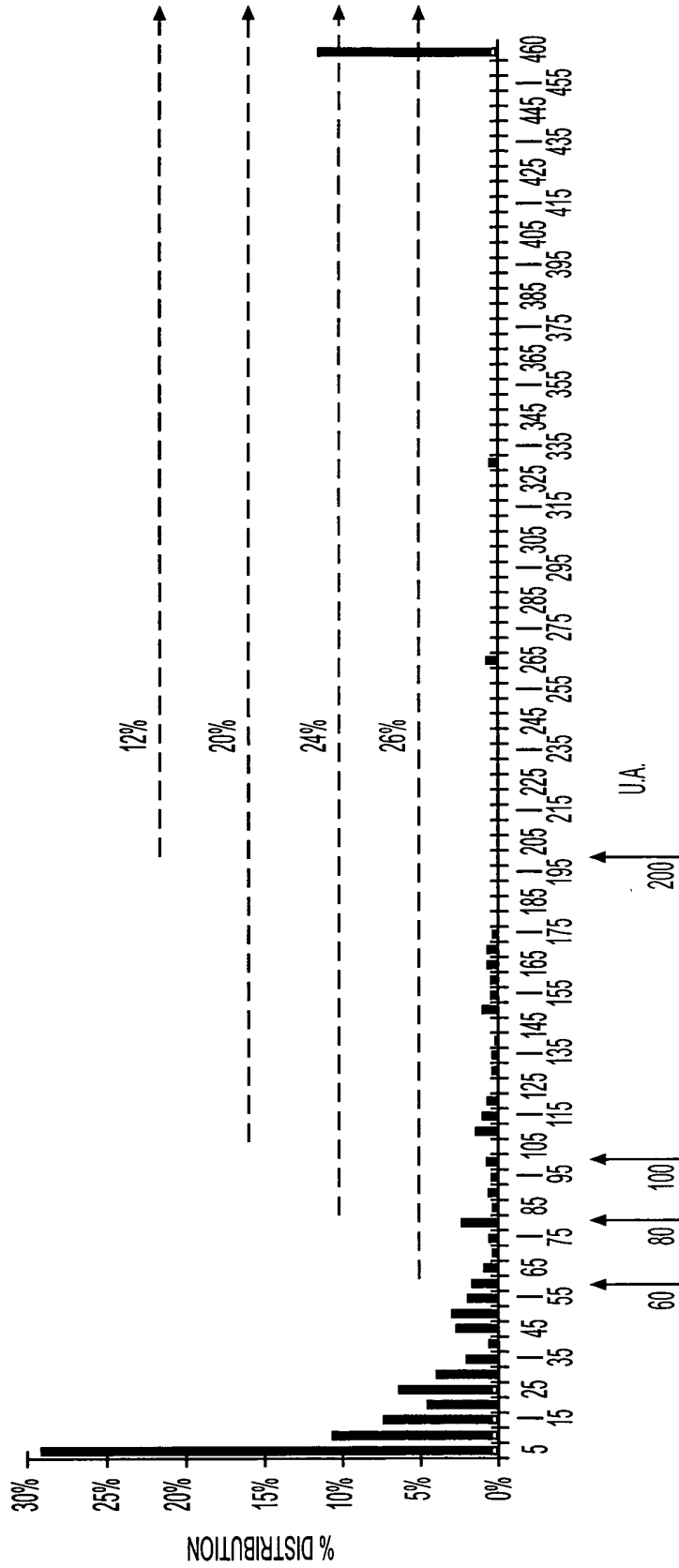


FIG. 9



Replacement Sheet

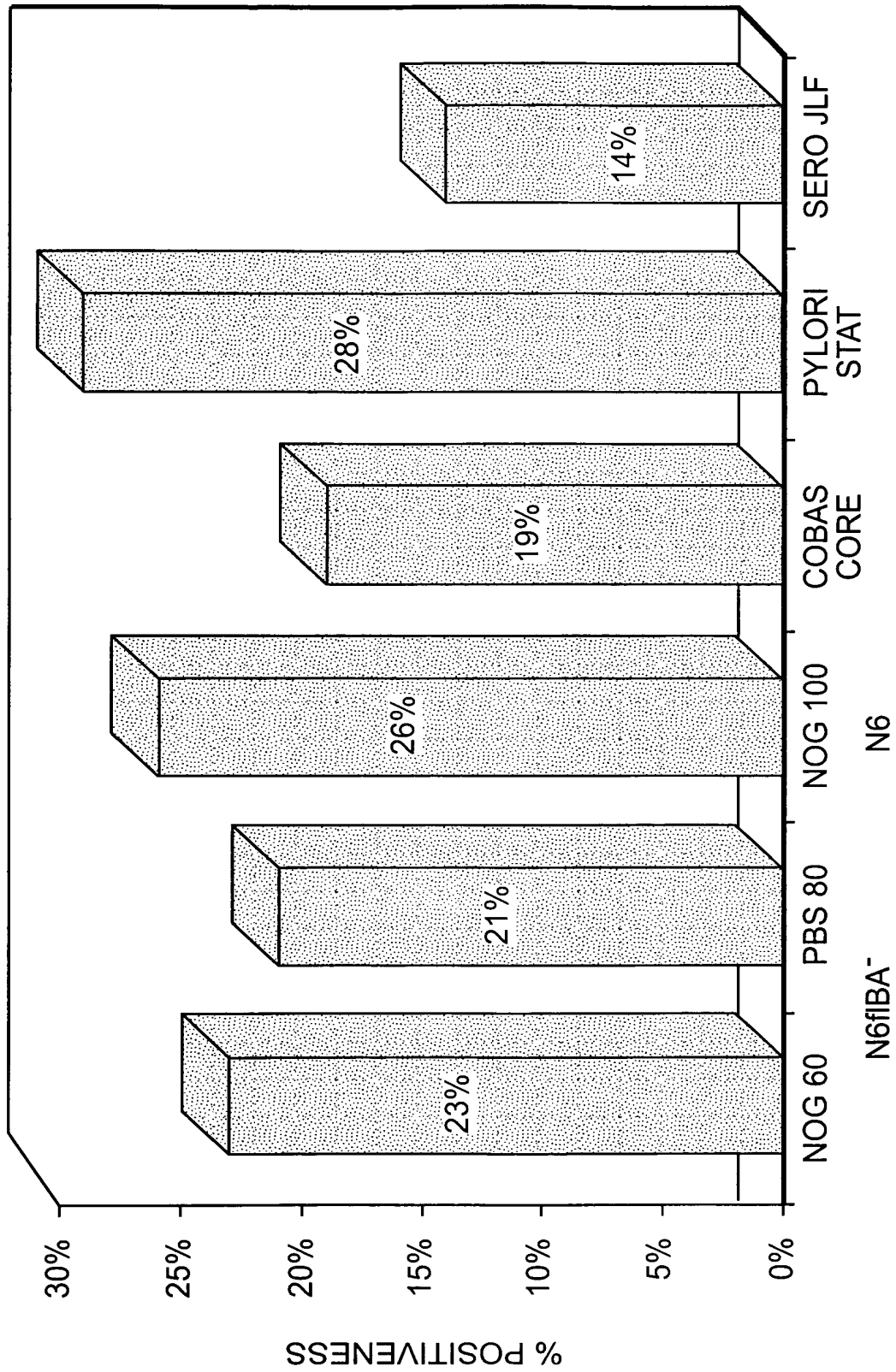


FIG. 10



Replacement Sheet

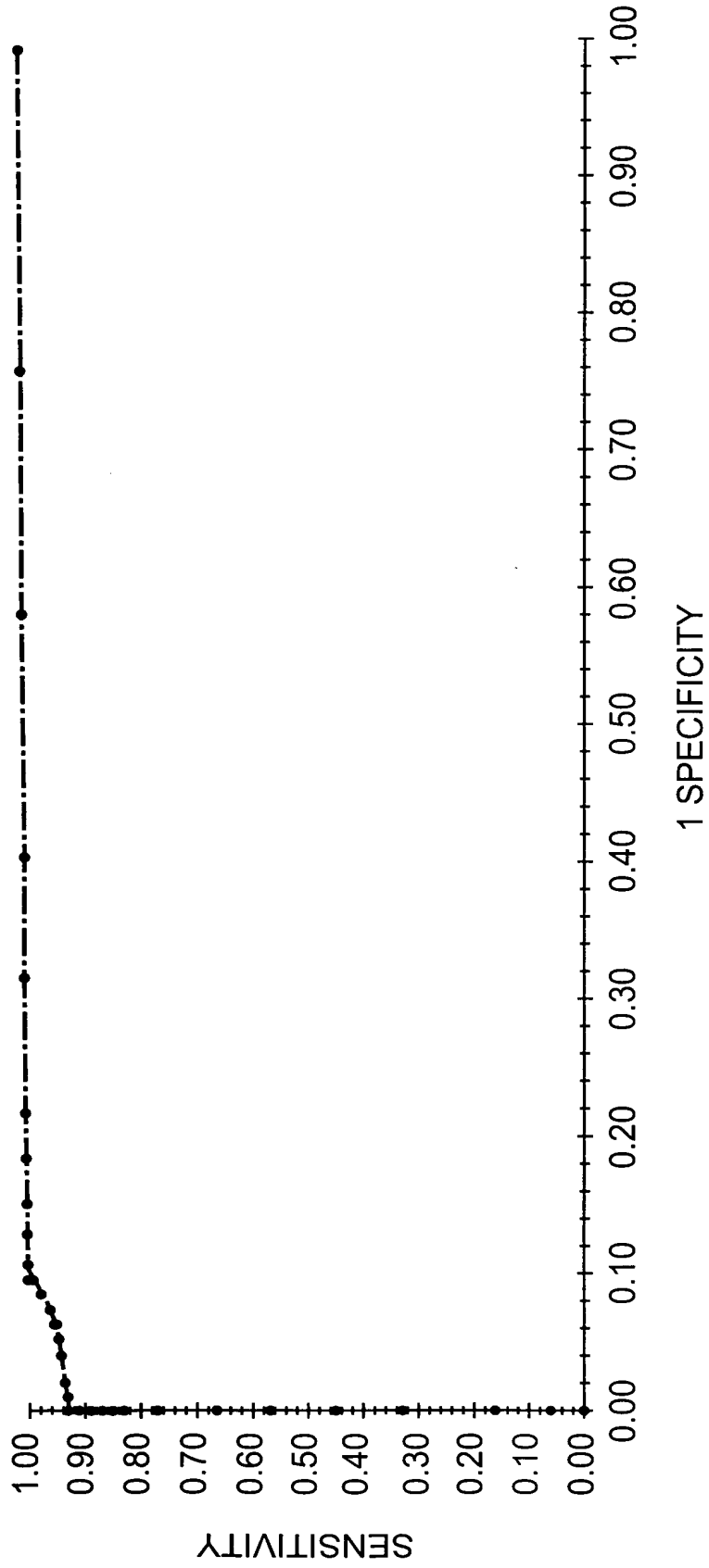
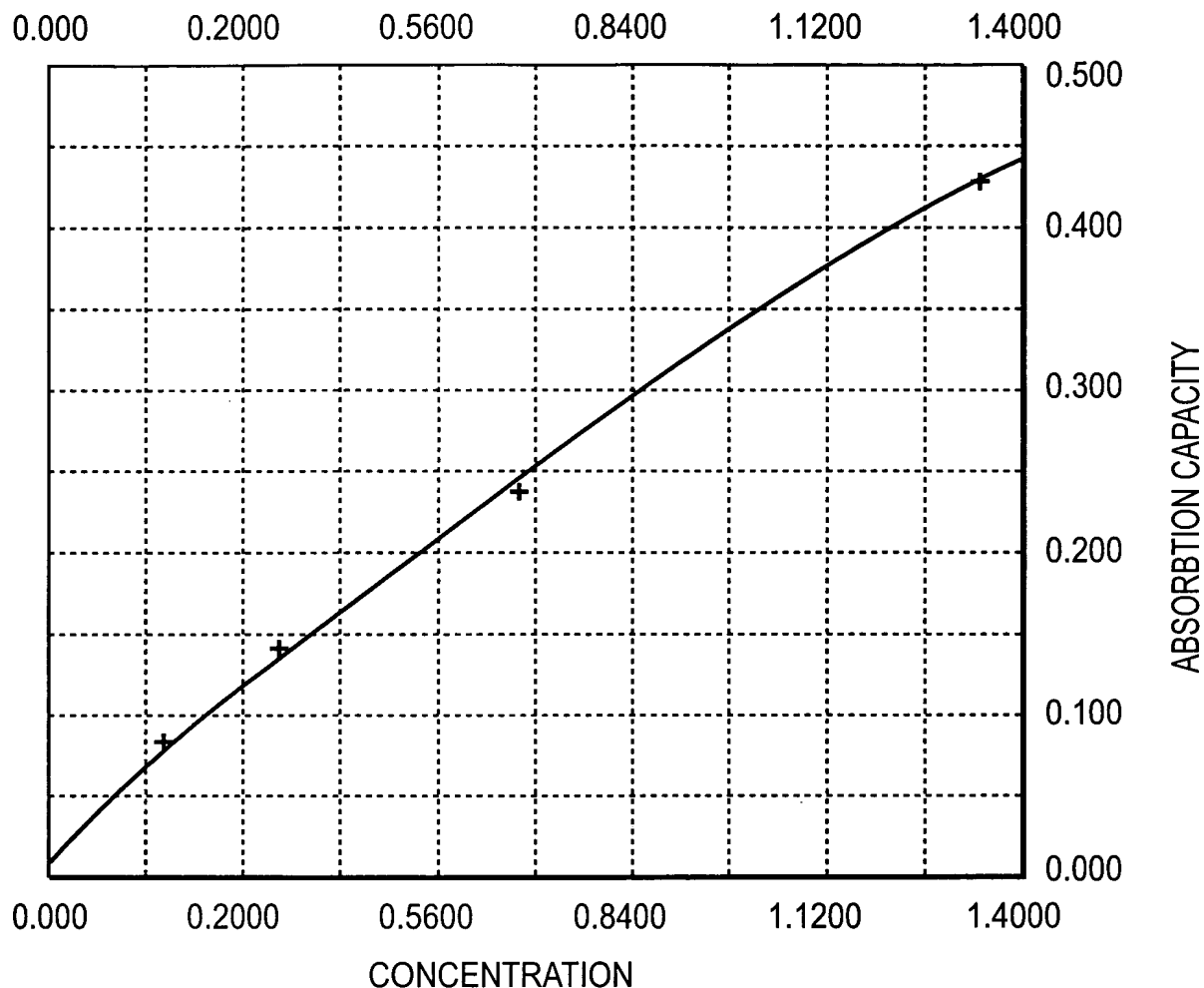


FIG. 11



Replacement Sheet



TYPE OF EXTRACT	DO @ 750nm	CONCENTRATION IN mg/ml
<u>GLYCINE</u> (AFTER CENTRIFUGATION FOR 15 min @ 3000 g)	0.028	0.284
<u>N-OCTYL-GLYCOSIDE</u>	0.087	1.004
<u>SUPERNATANT 1</u> (AFTER 1ST PBS WASHING)	0.059	0.844
<u>SUPERNATANT 2</u> (AFTER 2nd PBS WASHING)	0.015	0.1105

FIG. 12



Replacement Sheet

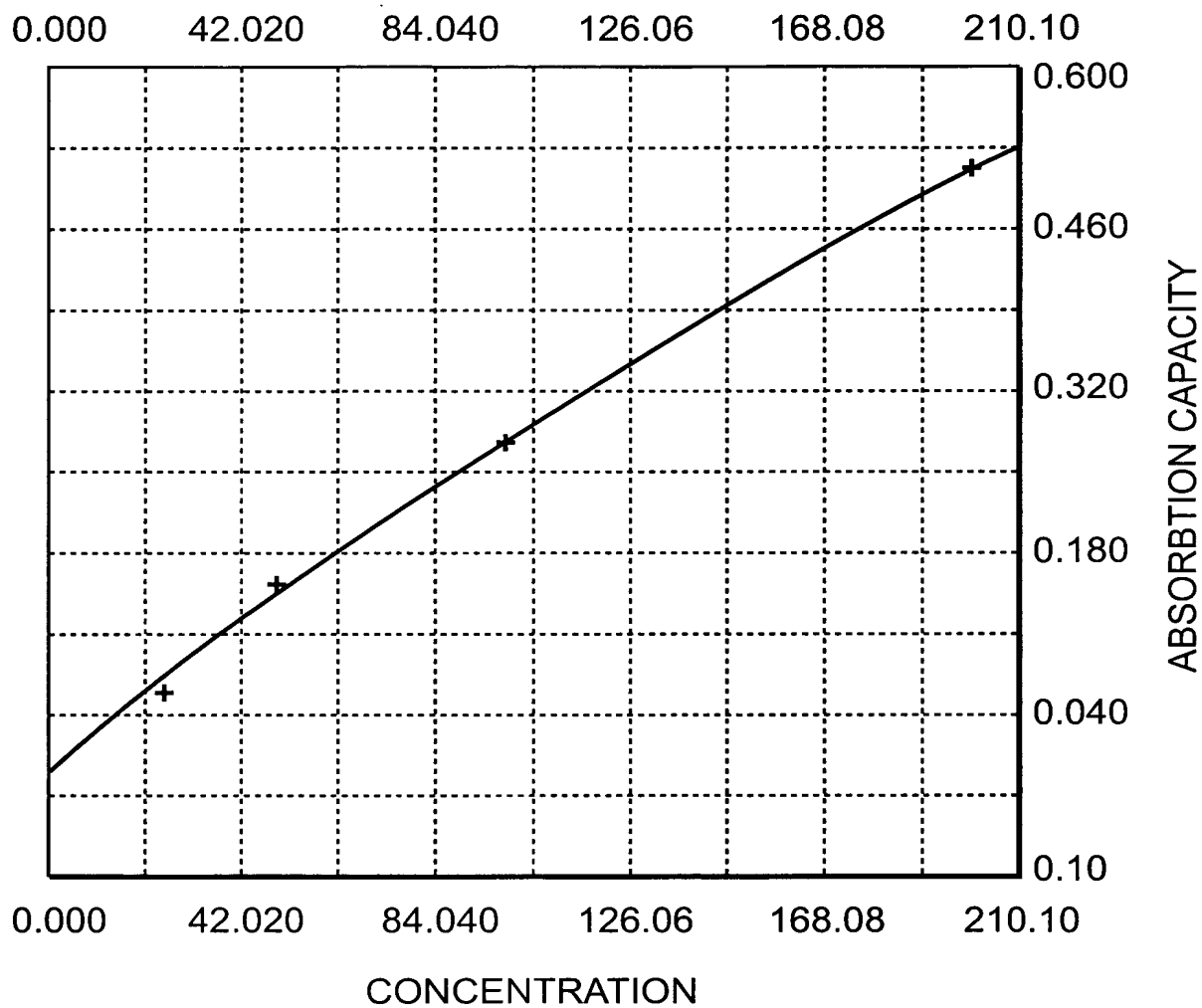


FIG. 13(A)



Replacement Sheet

TYPE OF EXTRACT	DO @ 760 nm	CONCENTRATION IN µg/ml
GLYCINE (AFTER CENTRIFUGATION FOR 15min @ 3000g)	0.279	202.86
<u>N-OCTYL-GLUCOSIDE</u>	0.243	873.99
<u>SUPERNATANT 1 (AFTER 1ST PBS WASHING)</u>	0.361	539.2
<u>SUPERNATANT 2 (AFTER 2ND PBS WASHING)</u>	0.218	77.875

TYPE OF EXTRACT	DO @ 760 nm	CONCENTRATION IN µg/ml
GLYCINE RESIDUE (AFTER 15 min OF CENTRIFUGATION AT 3000g)	0.099	297.5
GLYCINE RESIDUE (AFTER EXTRACTION)	0.093	2778.7
<u>N-OCTYL-GLUCOSIDE (AFTER EXTRACTION)</u>	0.275	972.0

FIG. 13B